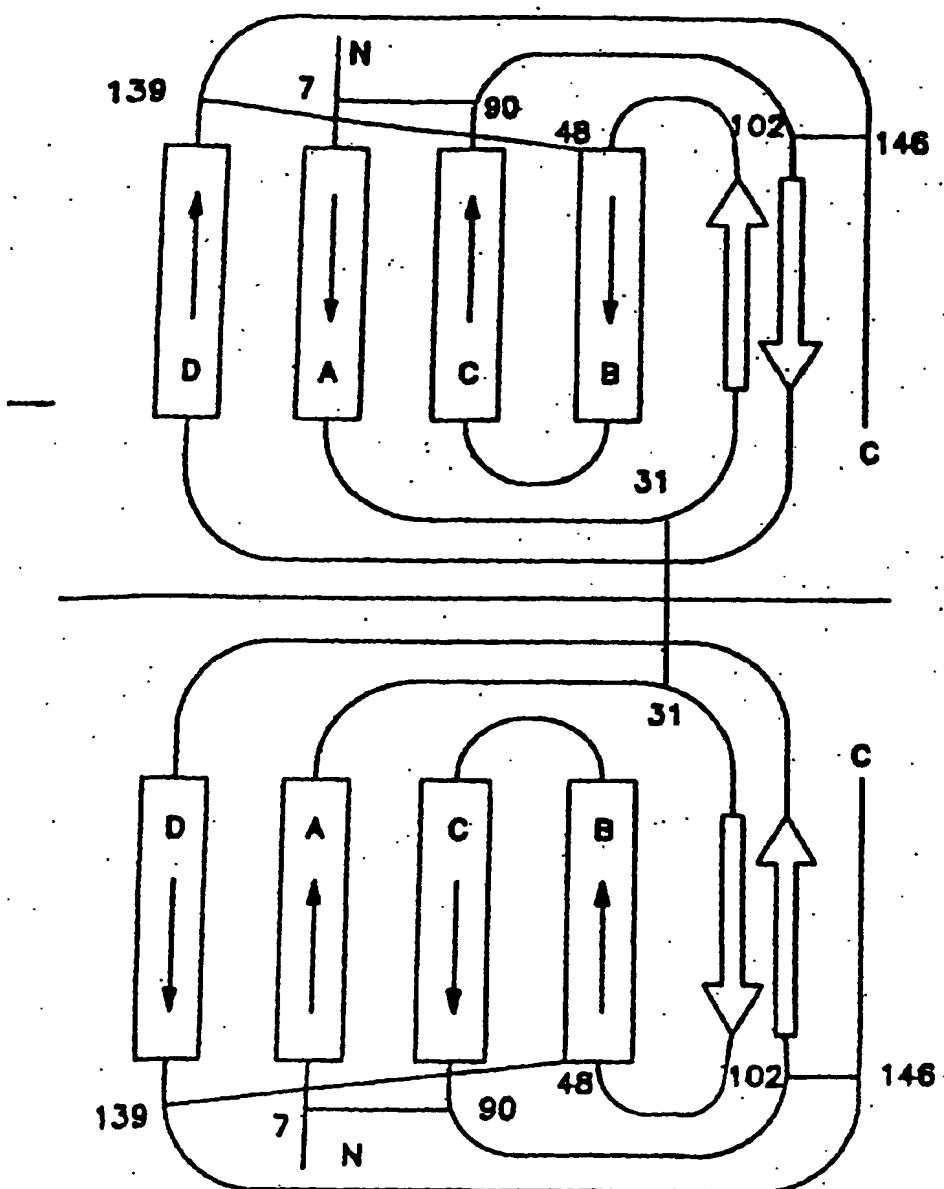


FIG. 1



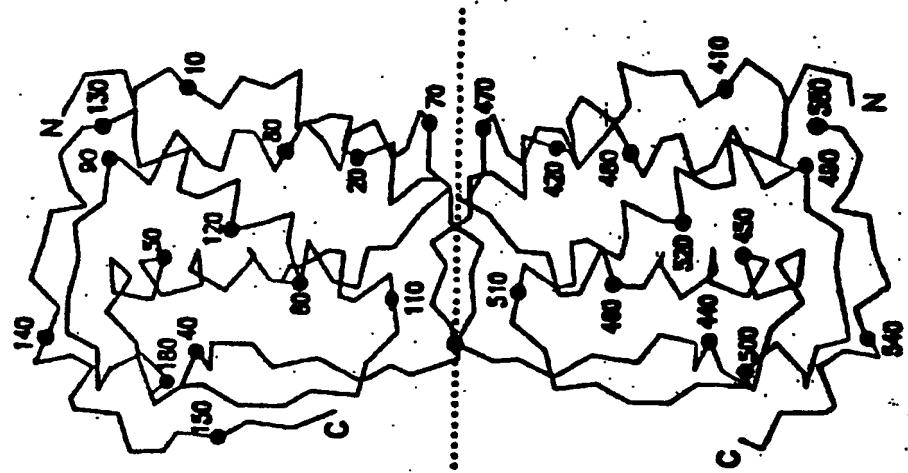


FIG. 3

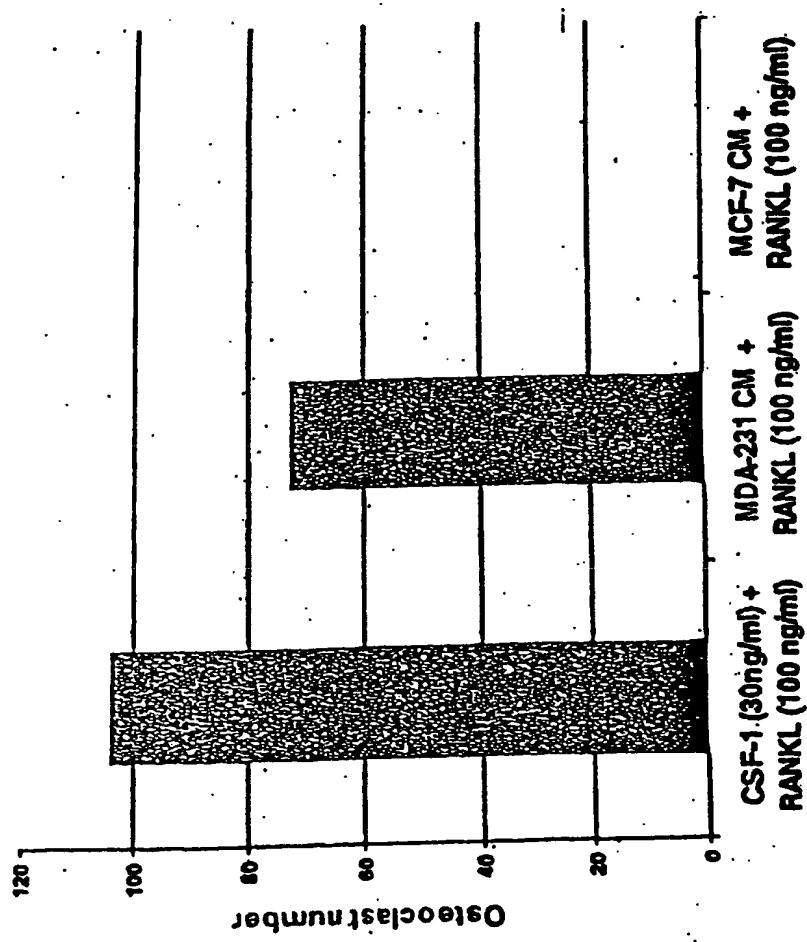


Fig. 4A

11. Light chain amine acid sequence:

1 [LLTQSPAILSVSPGERVSFSCRASOSIGTSIHWYQQRTNGSPRLIYKASESISGIPSRSFGSGCTDFTL.SINSVESEDIAIDYCYQQINSWPTTFGGGTKEIKRADAAPTVSIFPPSSE
2 .LTGGASAVCFLLNFYPKDINVKWKIDGSEERONGVILNSWTTDODSKDSTYSMSSTTLTKDYEYERHNSYTCATEATHKTSTSPIVKSFNBNEC
3

1.1 Heavy Chain amino acid sequence

[[[heavy chains]]] are generated:

III. *Intertidal Chironomid Fauna and its Significance*

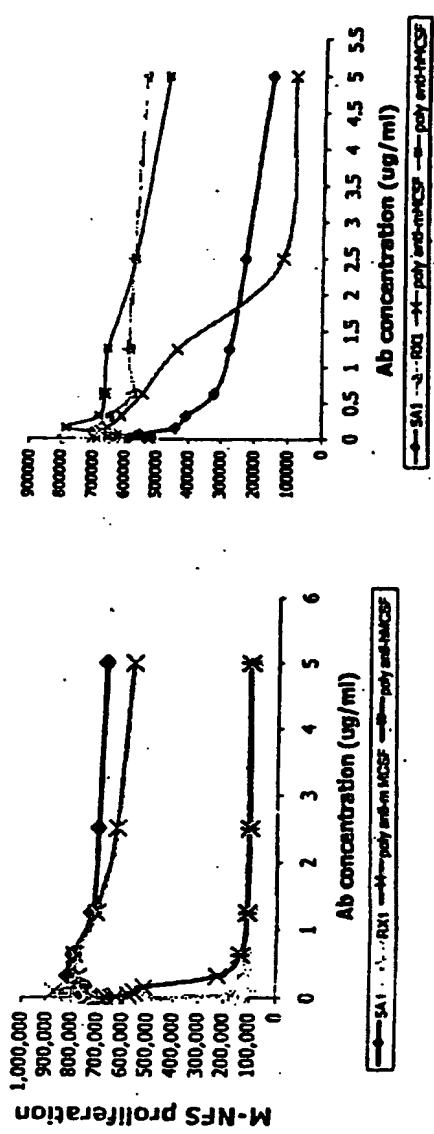
FIG. 4B

CHIR-R1X Light Chain Risk Assignments

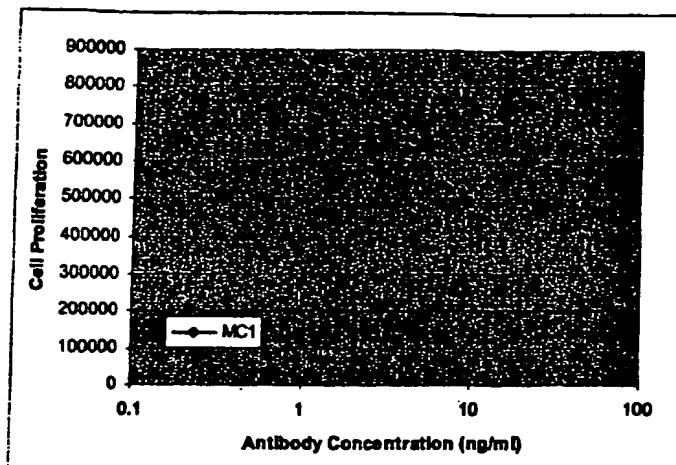
FIG. 4C

CHIR-RX1 Heavy Chain Risk Assignments

FIG. 5A



MC1 Neutralizes human MCSF activity



MC3 Neutralizes human MCSF activity

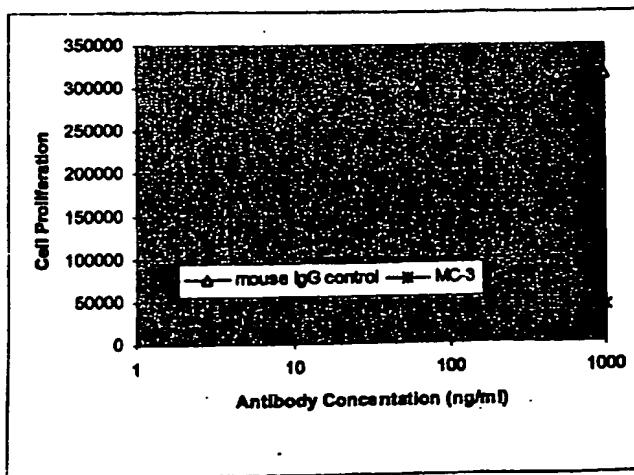


Fig. 6

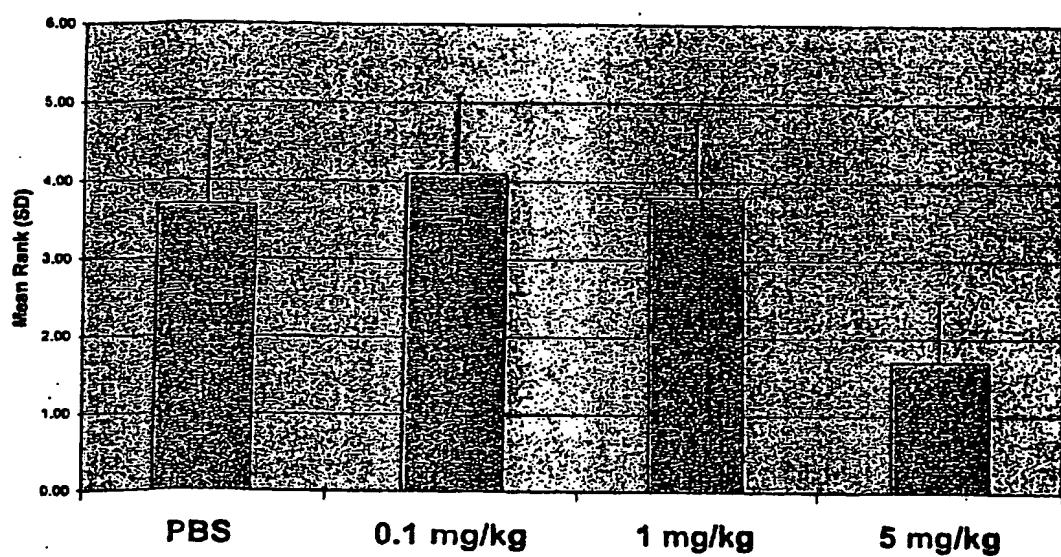


Fig. 7

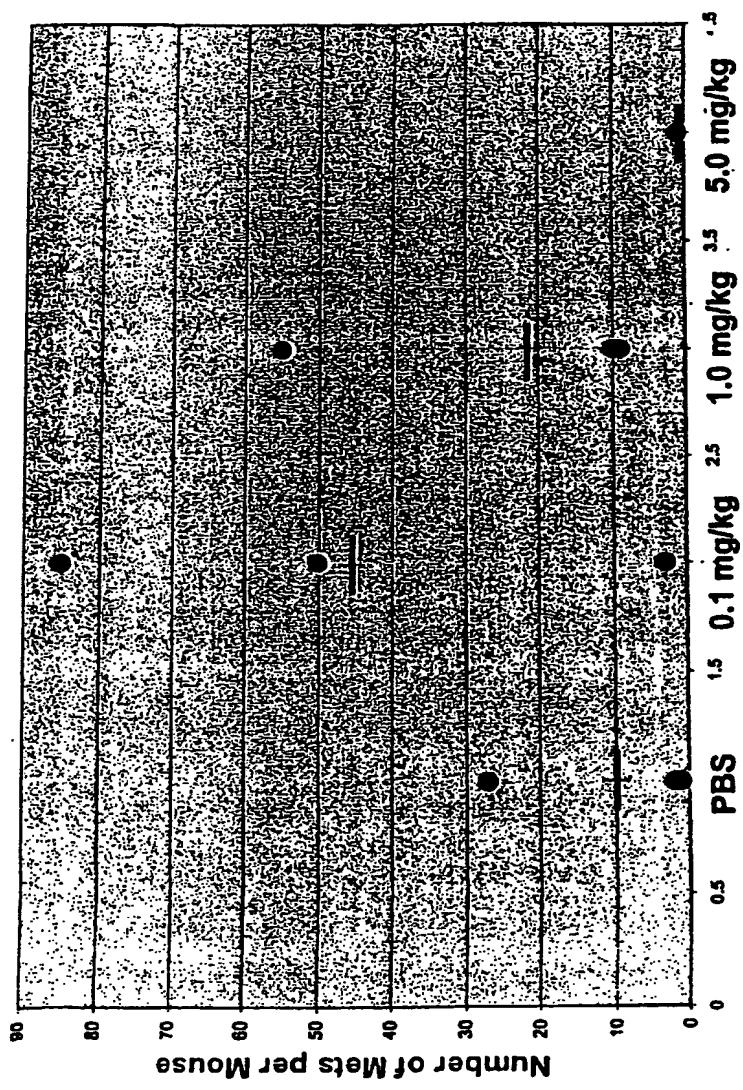
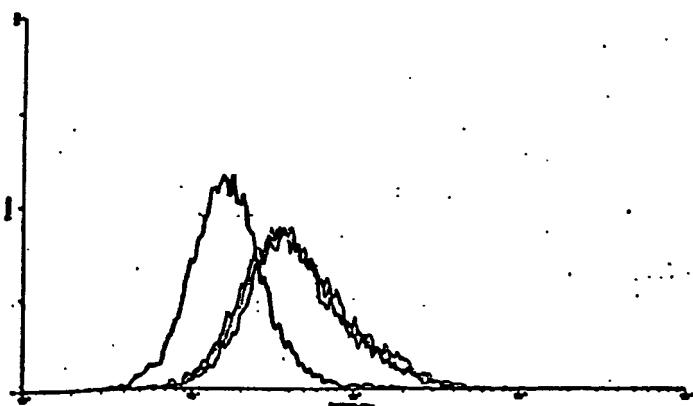


FIG. 8A**Binding of MCSF-specific antibody to breast cancer cell line MDA231**

Red: no antibody control
Black: M-CSF antibody 1 μ g/ml
Green: M-CSF antibody 10 μ g/ml
Blue: M-CSF antibody 50 μ g/ml

**FIG. 8B****Binding of MCSF-specific antibody to multiple myeloma cancer cell line ARH77**

Red: no antibody control
Green: M-CSF antibody 5 μ g/ml
Blue: control IgG2a 5 μ g/ml

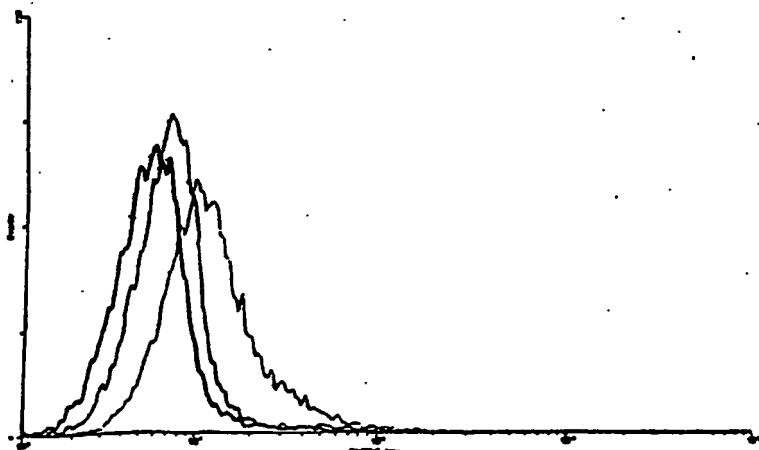


FIG. 9

Cancer Type	Cancer Status	Score 0	Score 1	Score 2	Score 3	Score 4	% with scores 3 or higher
adrenal	normal	10	5	5	0	0	0
basal cell	cancer	5	0	0	0	0	0
bladder	normal	6	1	2	1	0	10
brain	normal	17	1	2	0	0	0
breast	cancer	6	5	13	62	0	72
breast	normal	7	5	7	6	0	24
carcinooids	cancer	9	2	2	0	0	0
carcinooids (muscle)	cancer	1	0	1	0	0	0
choriocarcinoma	cancer	1	0	0	0	0	0
colon	normal	4	0	2	0	0	0
colon	cancer	9	0	1	4	0	27
fibrosarcoma	cancer	3	1	0	0	0	0
cellbladder	normal	2	1	0	1	0	25
germ cell	cancer	1	0	0	0	0	0
heart	normal	7	3	2	4	0	25
Kidney	normal	5	10	1	4	0	20
Kidney	cancer	8	1	0	3	0	25
leiomysarcoma	cancer	5	0	0	0	0	0
liver	normal	11	3	4	1	0	5
liver	cancer	5	3	0	3	0	27
lung	normal	18	0	1	0	0	0
lung	cancer	3	1	0	3	0	43
lymphoma	cancer	13	0	3	2	0	12
melanoma	cancer	7	0	2	5	0	36
melanoma (inflammation)	cancer	0	0	0	1	0	100
mesothelioma	cancer	6	0	0	0	0	0
neuroblastoma	cancer	1	0	0	0	0	0
ovary	normal	6	0	2	0	0	0
ovary	cancer	8	2	0	4	0	29
pancreas	normal	9	2	5	4	0	20
pancreas	cancer	8	1	0	3	0	25
prostate	normal	0	3	8	3	0	21
prostate	cancer	9	1	1	4	0	27
sercoma all	cancer	6	0	2	2	0	20
sercome	cancer	3	0	2	1	0	17
sercome (kidney)	cancer	3	0	2	1	0	17
seroma mfn	cancer	2	0	0	0	0	0
seminoma	cancer	3	0	0	0	0	0
small intestine	normal	2	1	0	1	0	25
spleen	normal	14	2	3	0	0	0
squamous cell	cancer	3	0	0	0	0	0
stomach	normal	3	2	2	1	0	13
stomach	cancer	7	1	1	1	0	10
teratoma	cancer	1	0	0	0	0	0
testis	normal	5	1	3	3	0	25
thyroid	normal	15	0	0	0	0	0
thyroid	cancer	6	2	1	2	0	16
undiff all	cancer	6	0	2	1	0	11
undif	cancer	5	0	2	0	0	0

Fig. 10

Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
1 5 10 15

Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
20 25 30

Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
35 40 45

Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
50 55 60

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
65 70 75 80

Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
85 90 95

Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
100 105 110

Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
115 120 125

Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
130 135 140

Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
145 150 155 160

Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
165 170 175

Glu Cys Ser Ser Gln Gly His Glu Arg Gln Ser Glu Gly Ser Ser Ser
180 185 190

Pro Gln Leu Gln Glu Ser Val Phe His Leu Leu Val Pro Ser Val Ile
195 200 205

Leu Val Leu Leu Ala Val Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg
210 215 220

Arg Ser His Gln Glu Pro Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro
225 230 235 240

Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg Gln Val Glu Leu Pro Val
245 250 255

Fig. 11

Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
 1 5 10 15
 Gly Ser Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
 20 25 30
 Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
 35 40 45
 Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
 50 55 60
 Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
 65 70 75 80
 Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
 85 90 95
 Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
 100 105 110
 Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
 115 120 125
 Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
 130 135 140
 Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
 145 150 155 160
 Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
 165 170 175
 Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
 180 185 190
 Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
 195 200 205
 Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
 210 215 220
 Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
 225 230 235 240
 Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser
 245 250 255
 Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
 260 265 270
 Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
 275 280 285
 Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
 290 295 300
 Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
 305 310 315 320
 Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Ser Met Gln Thr Glu
 325 330 335
 Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
 340 345 350
 Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly Thr Ala Leu Pro
 355 360 365
 Arg Val Gly Pro Val Arg Pro Thr Gly Gln Asp Trp Asn His Thr Pro
 370 375 380
 Gln Lys Thr Asp His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro
 385 390 395 400
 Gly Ser Pro Arg Ile Ser Ser Leu Arg Pro Gln Gly Leu Ser Asn Pro
 405 410 415
 Ser Thr Leu Ser Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly
 420 425 430
 Ser Val Leu Pro Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp
 435 440 445
 Arg Arg Ser Pro Ala Glu Pro Glu Gly Gly Pro Ala Ser Glu Gly Ala
 450 455 460
 Ala Arg Pro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly
 465 470 475 480
 His Glu Arg Gln Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser
 485 490 495
 Val Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val
 500 505 510
 Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro
 515 520 525
 Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr
 530 535 540
 Gln Asp Asp Arg Gln Val Glu Leu Pro Val

Fig. 12

Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
 1 5 10 15
 Gly Ser Leu Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
 20 25 30
 Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
 35 40 45
 Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
 50 55 60
 Ile Thr Phe Phe Val Asp Gln Glu Leu Lys Asp Pro Val Cys
 65 70 75 80
 Tyr Leu Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
 85 90 95
 Met Arg Phe Arg Asp Asn Thr Pro Asn Ala Ile Ala Ile Val Gln Leu
 100 105 110
 Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
 115 120 125
 Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
 130 135 140
 Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
 145 150 155 160
 Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
 165 170 175
 Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
 180 185 190
 Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
 195 200 205
 Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
 210 215 220
 Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
 225 230 235 240
 Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser
 245 250 255
 Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
 260 265 270
 Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
 275 280 285
 Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
 290 295 300
 Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
 305 310 315 320
 Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Ser Met Gln Thr Glu
 325 330 335
 Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
 340 345 350
 Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Gly His Glu Arg Gln
 355 360 365
 Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser Val Phe His Leu
 370 375 380
 Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val Gly Gly Leu Leu
 385 390 395 400
 Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro Gln Arg Ala Asp
 405 410 415
 Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg
 420 425 430
 Gln Val Glu Leu Pro Val

FIG. 13**5H4 heavy chain protein sequence:**

1 EIQLQQSGPE LVKTGTSVKI SCKASGYSFT GYFMHWVKQS HGKSLEWIGY
51 ISCYNGDTNY NQNFKGKATF TVDTSSSTAY MQFNSLTSQD SAVYYCAREG
101 GNYPAYWGQG TLVTVSAAKT TPPSVYPLAP GSAAQTNNSMV TLGCLVKGYF
151 PEPVTVTWNS GSLSSGVHTF PAVLQSDLYT LSSSVTVPSS TWPSETVTCN
201 VAHPASSTKV DKKIVPRDCG CKPCICTVPE VSSVFIFPPK PKDVLITLTLT
251 PKVTCVVVDI SKDDPEVQFS WFVDDVEVHT AQTQPREEQF NSTFRSVSEL
301 PIMHQDWLNG KEFKCRVNSA AFPAPIEKTI SKTKGRPKAP QVYTI PPPKE
351 QMAKDKVSLT CMITDFFPED ITVEWQWNGQ PAENYKNTQP IMDTDGSYFV
401 YSKLNVQKSN WEAGNTFTCS VLHEGLHNHH TEKSLSHSPG K

5H4 light chain protein sequence:

1 DIVMTQSHKF MSTSVGDRVT ITCKASQNVG TAVTWYQQKP GQSPKLLIYW
51 TSTRHAGVPD RFTGSGSGTD FTLTISDVQS EDLADYFCQQ YSSYPLTFGA
101 GTKLELKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVWKI
151 DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
201 STSPIVKSFN RNEC

FIG. 14

MC-1 heavy chain protein sequence:

```
1  EVKLVESGGG LVQPGGSLKL SCATSGFTFS DYYMYWVRQT PEKRLEWVAY
 51  ISNGGGSTYY PDTVKGRFTI SRDNAKNTLY LQMSRLKSED TAMYYCARQG
101  SYGYPPFAYWG QGTLVTVSAA KTTAPSVYPL APVCGDTTGS SVTLGCLVKG
151  YFPEPVTLW NSGSLSSGVH TFPAVLQSDL YTLSSSVTVT SSTWPSQSIT
201  CNVAHPASST KVDKKIEPRG PTIKPCPPCK CPAPNLLGGP SVFIFPPKIK
251  DVLMISLSPV VTCVVVDVSE DDPDVQISWF VNNVEVHTAQ TQTHREDYNS
301  TLRVVSALPI QHQDWMSGKE FKCKVNNKDL PAPIERTISK PKGSVRAPQV
351  YVLPPEEEM TKKQVTLTCM VTDFMPEDIY VEWTNNNGKTE LNYKNTEPVL
401  DSDGSYFMYS KLRVEKKNWV ERNSYSCSVV HEGLHNHHTT KSFSRTPGK
```

MC-1 light chain protein sequence:

```
1  AIQMTQTTSS LSASLGDRVT ISCSASQGIS NYLNWYQQKP DGTVKLLIYY
 51  TSSLHSGVPS RFSGSGSGTD YSLTISNLEP EDIATYYCQQ YSKLPWTFGG
101  GTKLEIKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVWKI
151  DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
201  STSPIVKSFN RNEC
```

FIG. 15**MC-3 heavy chain protein sequence:**

1 DVQLQESGPG LVKPSQSLSL TCTVTGYSIT SDYAWNWIHQ FPGNKLEWMG
51 YISYSGSTSY NPSLKSRI SI TRDTSKNQFF LQLNSVTTED TATYYCARLE
101 TWLFDYWGQQ TTLTVSSAKT TPPSVYPLAP GCGDTTGSSV TLGCLVKGYF
151 PESVTVTWNS GSLSSSVHTF PALLQSGLYT MSSSVPSS TWPSQTVTCS
201 VAHPASSTTV DKKLEPSGPI STINPCPPCK ECHKCPAPNL EGGPSVPIFP
251 PNIKDVLMIS LTPKVTCVVV DVSEDDPDVQ ISWFVNNVEV HTAQQTQTHRE
301 DYNSTIRVVS TLPIQHQDWG SGKEFKCKVN NKDLPSPIER TISKIKGLVR
351 APQVYILPPP AEQLSRKDVS LTCLVVGFNP GDISVEWTSN GHTEENYKDT
401 APVLDSDGSY FIYSKLNMKT SKWEKTDTSFS CNVRHEGLKN YYLKKTISRS
451 PGLDLDDICA EAKDGELEDGL WTTITIFISL FLLSVCYSAS VTLFKVKWIF
501 SSVVELKQKI SPDYRNMIGQ GA

MC-3 light chain protein sequence:

1 DILLTQSPAI LSVSPGERVS FSCRASQSIG TSIHWYQQRT NGSPLRLLIK
51 ASESISGIPS RFSGSGSGTD FTLSINSVES EDIADYYCQQ SNSWPPTTFGG
101 GTKLEIKWAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVWKWI
151 DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
201 STSPIVKSFN RNEC

FIG. 16A

For heavy chain CDR1:

	1	
H_CDR1_5H4	(1)	-G Y FMH
H_CDR1_MC-1	(1)	- Y YMY
H_CDR1_CHIR-RX1	(1)	SDY Y
H_CDR1_MC-3	(1)	SDY Y
Consensus	(1)	SDYAWN

For heavy chain CDR2:

	1	17	
H_CDR2_5H4	(1)	YIS C NG DTNY Q QNF K G	
H_CDR2_MC-1	(1)	YIS N GGG TYYPD K G	
H_CDR2_CHIR-RX1	(1)	YIS- SG TSYNP SL K	
H_CDR2_MC-3	(1)	YIS- SG TSYNP SL K	
Consensus	(1)	YIS YSGSTS NP SLKS	

For heavy chain CDR3:

	1	
H_CDR3_5H4	(1)	-- G NYPAY
H_CDR3_MC-1	(1)	QGS W PAY
H_CDR3_CHIR-RX1	(1)	-F Y HAM Y
H_CDR3_MC-3	(1)	--LET L Y
Consensus	(1)	DYGW FDY

FIG. 16B

For light chain CDR1:

	1	11
L_CDR1_5H4	(1) RASON	PP
L_CDR1_MC-1	(1) SASOG	SNY
L_CDR1_CHIR-RX1	(1) RASQ	SI
L_CDR1_MC-3	(1) RASQ	SI
Consensus	(1) RASQ	SIGTSIH

For light chain CDR2:

	1
L_CDR2_5H4	(1) STRH
L_CDR2_MC-1	(1) SSLH
L_CDR2_CHIR-RX1	(1) RAS
L_CDR2_MC-3	(1) RASE
Consensus	(1) YTSE

For light chain CDR3:

	1
L_CDR3_5H4	(1) QQ
L_CDR3_MC-1	(1) QO
L_CDR3_CHIR-RX1	(1) QGIN
L_CDR3_MC-3	(1) QGSN
Consensus	(1) QQYSSWPTT

FIG. 17

Neutralization Activities of Intact mAbs vs. Fab

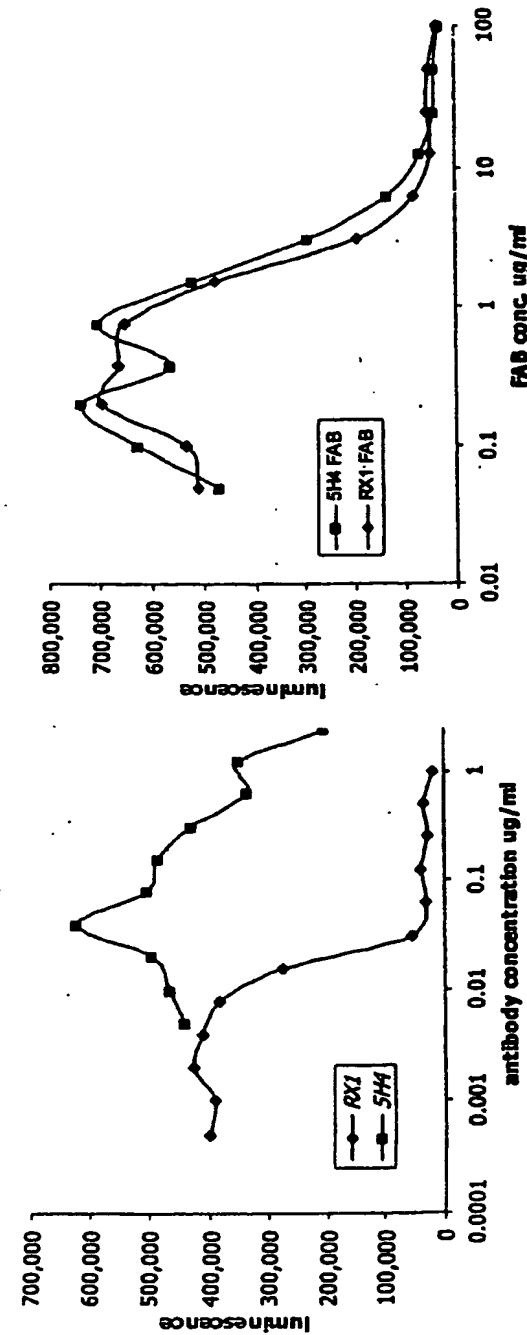
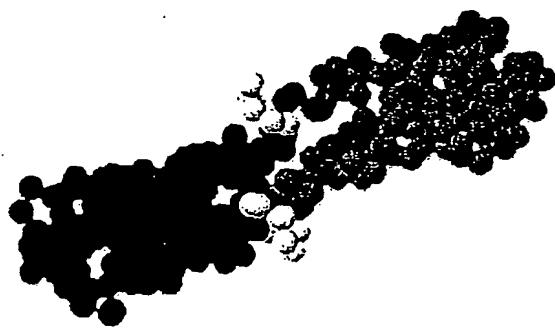
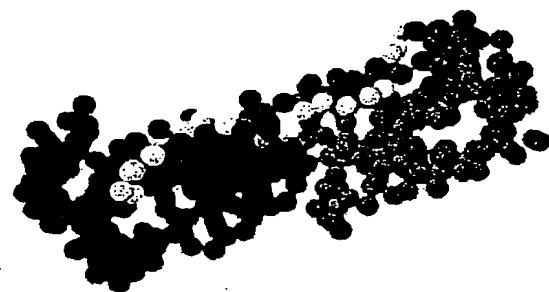


FIG. 18

MCSF Structure with RX1 Epitopes HighlightedRX15H4MC3

R₉₈FRDNTPN₁₀₅

I₆₅TFEFVDQE₇₃

F₁₃₈YETPLQ₁₄₄

FIG. 19A

FIG. 19B**Low Risk Heavy Chain Vs. Kabat Vh2 Consensus:****Protein Seq:**

DVQLQESGPGLVKPSQTLSLTCTVTDYSITSVDYAWNWRQFPGKLEWMGYISYSGSTSYNPSLKSRTISRDTSKNQFSLQLNSVTAADTA
YWGGTIVTVSS

DNA Seq:

GACGTACAACCTCAAGAATCTGGCCCAGGTCTCGTCAAACCTCTCTCAAACTCTCACTCACCTGCACTGTTACTGACTACTCTATTACATCCGACTACGGCTT
GGAAACTGGATCCGACAATTCTGGTAAAAAAACTCGAATGGATGGTTATTCTTACTCTGGCTCACCTCTACAATCCTCTCTGAATACGGCATCAC
AATTTCGGCGCATACCTCTAAAAATCAATTTCACACTCCAACCTCAATTCTGTTACCGCCGGATACTGCCACCTACTCTGCTCTTTGACTACGGCTCAC
CCATGGATTATTGGGACAGGGTACTACCGTTACCGTAAGCTCA

Low Risk + Moderate Risk Heavy Chain Vs. Kabat Vh2 Consensus:**Protein Seq:**

QVQLQESGPGLVKPSQTLSLTCTVSDYSITSVDYAWNWRQFPGKGLEWMGYISYSGSTSYNPSLKSRTISRDTSKNQFSLQLNSVTAADTA
YWGGTIVTVSS

DNA Seq:

CAAGTTCAACCTCAAGAATCAGGGCCCCGGACTCGTTAACCCCTCTCAAACCTCTGCACTGTATCCGATTACTCTTACTCTCAGACTACGGCTTG
GAACTGGATCAGACAATTCCGGAAAAGGACTCGAATGGATGGGATAATCTCTTACTCTGGCTCAACCTCTCTCAAACCCCTCTCGAAATCCTCGAATAAC
AATCTCACGGCATACTCTAAAAATCAATTCTCAACTTAACCTCAACTTAACCTCGTTACTGCGCGGACACTGCCGTTACTCTGCTTACGGTCAACTGTCA
CTATGGATTATTGGGACAAAGGAACCTACCGTCACTGTCACTGTCA

FIG. 20A

Light Chain

FIG. 20B**Low Risk Light Chain Vs. Kabat Vκ3 Consensus:****Protein Seq:**

EIVLTQSPGTLSVSPGERVTFSRASQSIGTSIHWWYQQKTGQSPRLIKYASERISGIPDRFSGSQGTDFTLTISRVESEDFA
DYYCQQQINSWPPTFGQGTKLEIKRT

Nucleotide Seq:

GAAATAGTCCTAACCCAAATCTCCCCGAACCCCTCTCAGTATCTCCCCGGAAACGGAGTAACCTTTCATGTAGAGCCATCCC
GGTATCAGCAGAAAACAGGTCAATCCCACGGCTCTTATAAAATATGCCATCAGAAAGAATATCAGGCAATTCCAGACAGATT
ACAGACTTCACACTACAATTTCGGCGTGAATCCGAAGACTATTACTGCCAAACTCAACTCATGGCCTACTACTTCGGTCAAGGC
AAACTCGAAAATTAAACGTACG

Low Risk + Moderate Risk Light Chain Vs. Kabat Vκ3 Consensus:**Protein Seq:**

EIVLTQSPGTLSVSPGERVTFSRASQSIGTSIHWWYQQKTGQAPRLIKYASERATGIPDRESGSQGTDFTLTISRVESEDFA
DYYCQQQINSWPPTFGQGTKLEIKRT

Nucleotide Seq:

GAAATAGTTTACTCAATCCCCGGTACACTTCTCAGTTGGCAGAGGATCACAATCAATCGGGCACTTCAATTCAATT
GGTATCAACAAAACAGGACAGGGCCACAGGCAATCCAGACAGATTTCAGGTTCAGGATTCAGGCA
ACGGATTCACTACAATTCAGACTTGCAGATTACTATTGTCAACAAATAAACAGCTGGCCCACATTCGGACAAAGGCACA
AAACTCGAAAATTAAACGTACG

FIG. 21A

Light Chain – Changes back to Murine

FIG. 21B

Low Risk Light Chain Vs. Kabat V_k3 Consensus; AA54 changed back to murine:**Protein Seq:**

EIVLTQSPGTLSVSPGERVTFSRASQSIGTSIHWYQQKTKQSPrLLIKYASESISIGIPDRFSGSQGTDFTLTISRVESEDFA
DYYQQQINSWPTTFGQGTKEIKRT

Nucleotide Seq:

GAAATAGTCCTTACCAATCTCCCGGAACCCCTCTCAGTATCTCCGGAAACGAGTAACCTTTCATGTAGAGCATCCCAATCGGCAC
TTCAATTCTCAATGGTCAATCCACGGCTCTTATAAAATATGCAATCAGAATCAATTCTGGCATCCAGACAGATTTCA
GGATTCACACTTACAATATCCAGAGTCGAATTACTATTGTCAACAAATAAACAGCTGGCCCAC
ACTCGAAATTAAACGTACG

Low Risk + Moderate Risk Light Chain Vs. Kabat V_k3 Consensus; AA54, 55, 56 changed back to murine:**Protein Seq:**

EIVLTQSPGTLSVSPGERVTFSRASQSIGTSIHWYQQKTKQSPrLLIKYASESISIGIPDRFSGSQGTDFTLTISRVESEDFA
DYYQQQINSWPTTFGQGTKEIKRT

Nucleotide Seq:

GAAATAGTCCTTACTCAATCCCCGGTACACTCTCAGTTCCAGGGCAACGGCTCACITTTCTGGAGAGCATCACAATCAATCGGCAC
TTCAATTCTCAATGGCATCCAGACAGATTTCAATTAAATATGCAATCAGAATCAATTCTGGCATCCAGACAGATTTCA
GGATTCACACTTACAATATCCAGAGTCGAATTACTATTGTCAACAAATAAACAGCTGGCCCAC
ACTCGAAATTAAACGTACG

FIG. 22A

Light Chain – Changes based on HK6 2-1-1(A14)

FIG. 22B**Low Risk Light Chain vs. VK6 Subgroup 2-1-(1) A14:****Protein Seq:**

DIVLTQSPAFLSVTPGEKVTFTCQASQSIGTSIHWWYQQKTDQSPRLLIKYASESISGIPSRSGSGTDFTLTISSVEAEDAADYYCQQI

Nucleotide Seq: Not synthesized**Low Risk + Moderate Risk Light Chain vs. VK6 Subgroup 2-1-(1) A14:**

DIVLTQSPAFLSVTPGEKVTFTCQASQSIGTSIHWWYQQKTDQAPKLLIKYASESISGIPSRSGSGTDFTLTISSVEAEDAADYYCQQI
NSWPTTGGGTKEIKRT

Nucleotide Seq:

GACATAGTTCTCACACAAATCACCCAGCATTCAGTTACACCCGGGAAAAAGTAACCTTACCTGTCAGGGCTCTCAATCTATCGGCACCTCTATTCACT
GGTATCAACAAAACCGATCAAGCTCTAAACTCTCATATAAAATACGCCATCCGAATCCAATCCCCTCCGGTATCTCCGGTCAAGGCTCCGGCTCCGGCA
CAGATTTCACCCCTTACCAATTAGCTCAGTTGAGCTGAAGCCGAAGACGCCAGCTGATTACTACTGTCAACAAAATAAACTCATGGCCCACTACTTCCGGGGCGGCACTA
AACTCGAAATAAAACGTACG

FIG. 23A

Murine RX-1 Light Chain:
DILITQSPAILSVPGERVFSCRASQSIGTSIHWYQORTNGSPRLLIKYASESISIGSIPSRFSGSGCTDFTLSINSVESEDIA

LEIKRA

RX1 KV	(1)	DILITQSPAILSVPGERVFSCRASQSIGTSIHWYQORTNGSPRLLIKYASESISIGSIPSRFSGSGCTDFTLSINSVESEDIA
Consensus Germline LC		Y-----IHYQQRTNGSPRLLIKYASESISIGSIPSRFSGSGCTDFTLSINSVESEDIA
hVK I Consensus	(1)	DIQMTQSPSSLSAVGDRVTITCRASQSIGTSIHWYQORTNGSPRLLIKYASESISIGSIPSRFSGSGCTDFTLSINSVESEDIA
hVK II Consensus	(1)	DIVMTQSPPLSLPVTGEPASISCRSSQSLIHSQDGXXYLNWYLOQKPGQSPQLLIYXAS
hVK III Consensus	(1)	EIVLTQSPGTLSLSPGERATLSCRASQSIGTSIHWYQORTNGSPRLLIKYASESISIGSIPSRFSGSGCTDFTLSINSVESEDIA
hVK IV Consensus	(1)	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKILLIYXAS
hVK V Consensus	(1)	ETTILTQSPAFMSATPGDKVNISSCKASQDIDDD-----IHYQQRTNGSPRLLIKYASESISIGSIPSRFSGSGCTDFTLSINSVESEDIA
hVK VI Consensus	(1)	EIVLTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKILLIYXAS

LIGHT CHAIN amino half

RX-1 DILITQSPAILSVPGERVFSCRASQSIGTSIH-----WYQORTNGSPRLLIKYAS

pos... 10 20 abcdef 30 40 50

Kabat:

HK1...DIQMTQSPSSLSAVGDRVTITCRASQSIGTSIH-----WYQORTNGSPRLLIKYAS
HK2...DIVMTQSPPLSLPVTGEPASISCRSSQSLIHSQDGXXYLNWYLOQKPGQSPQLLIYXAS
HK3...EIVLTQSPGTLSLSPGERATLSCRASQSIGTSIH-----WYQORTNGSPRLLIKYAS
HK4...DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKILLIYXAS

Germline Consensus (with JK4):

hVK1 DIQMTQSPSSLSAVGDRVTITCRASQSIGTSIH-----IHYQQRTNGSPRLLIKYAS
hVK2 DIVMTQSPPLSLPVTGEPASISCRSSQSLIHSQDGXXYLNWYLOQKPGQSPQLLIYXAS
hVK3 EIVLTQSPGTLSLSPGERATLSCRASQSIGTSIH-----VSSSYLAWYQQKPGQAPRLLIYXAS
hVK4 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKILLIYXAS
hVK5 ETTILTQSPAFMSATPGDKVNISSCKASQDIDDD-----DMNHYQQKPGEAIFIQEAT
hVK6 EIVLTQSPDFQSVTPKEKVITCRASQSIG-----SSLHWYQQKPDQSPKILLIYXAS

FIG. 23B

LIGHT CHAIN carboxy half

RX-1 ESIISGIPSRFSGSGSGTDFTLISNSVSESEDIAVYCCQINSWPT-----TFFGGTKLEI-KRA

pos... 60_ 70_ 80_ 90_ abcdef 100_ a

Kabat:

HK1...XLXSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQXXXPE-----XTFGQGTKVEI-KRT
 HK2...NRXSGVPDRFSGSGSGTDFTLKISRVEAEDGVVYCCMQAXQXPR-----XTFGQGTKVEI-KRT
 HK3...SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSPP-----XTFGQGTKVEI-KRT
 HK4...TRESGVVPDRFSGSGSGTDFTLTISLQAEQDVAVYYCQQYYSTP-----XTFGQGTKVEI-KRT

Germline Consensus (with JK4) :

hVK1 SIQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTP-----LTFGGGTKVEI-KRT
 hVK2 YRASGVVPDRFSGSGSGTDFTLKISRVEAEDGVVYCCMQRIEFP-----LTFGGGTKVEI-KRT
 hVK3 SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSPP-----LTFGGGTKVEI-KRT
 hVK4 TRESGVVPDRFSGSGSGTDFTLTISLQAEQDVAVYYCQQYYSTP-----LTFGGGTKVEI-KRT
 hVK5 TLVPGIPPRFSGSGSGTDFTLTINNIESDAAYYFCLOHDNFP-----LTFGGGTKVEI-KRT
 hVK6 QSFSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSSL-----LTFGGGTKVEI-KRT

FIG. 24A

Murine RX-1 Heavy Chain:
DVQLQESGPGLVKPSQSLSLITCTVTDYSITSVDYAWNWRQFPGNKLEMMGYISYSGSTSYNPSLKSRSISITRDTSKNQFFLQLNSVTTEDTATYYC
ASFDFYAHAMDYWGQGTSTVSS

RX-1 VH
 Consensus Germline
 hVH I Consensus (1) D VQQLQESGPGLVKPSQSLSLITCTVTDYSITSVDYAWNWRQFPGNKLEMMGYISYSGSTS --- YNPSLKSRSISITRDTSKNQFFLQLNSVTTEDTATYYC
 hVH II Consensus (1) QVQLQESGPGLVKPSQSLSLITCTVTDYSITSVDYAWNWRQFPGNKLEMMGYISYSGSTS --- YNPSLKSRSISITRDTSKNQFFLQLNSVTTEDTATYYC
 hVH III Consensus (1) QVQLKESGPGLVKPSQSLSLITCTVTDYSITSVDYAWNWRQFPGNKLEMMGYISYSGSTS --- YNPSLKSRSISITRDTSKNQFFLQLNSVTTEDTATYYC
 hVH IV Consensus (1) E VQQLQESGPGLVKPSQSLSLITCTVTDYSITSVDYAWNWRQFPGNKLEMMGYISYSGSTS --- YNPSLKSRSISITRDTSKNQFFLQLNSVTTEDTATYYC
 hVH V Consensus (1) QVQLQESGPGLVKPSQSLSLITCTVTDYSITSVDYAWNWRQFPGNKLEMMGYISYSGSTS --- YNPSLKSRSISITRDTSKNQFFLQLNSVTTEDTATYYC
 hVH VI Consensus (1) E VQQLQESGPGLVKPSQSLSLITCTVTDYSITSVDYAWNWRQFPGNKLEMMGYISYSGSTS --- YNPSLKSRSISITRDTSKNQFFLQLNSVTTEDTATYYC
 hVH VII Consensus (1) QVQLQESGPGLVKPSQSLSLITCTVTDYSITSVDYAWNWRQFPGNKLEMMGYISYSGSTS --- YNPSLKSRSISITRDTSKNQFFLQLNSVTTEDTATYYC

HEAVY CHAIN amino half

DVQLQESGPGLVKPSQSLSLITCTVTDYSITSVDYAWN-WIRQFPGNKLEMMGYIS---YSGST

pos ...	10	20	30	ab	40	50	abc
---------	----	----	----	----	----	----	-----

Kabat:

HH1	... X	VOLVQSGAEVVKPGXSVKVSCKASGYTFXSIXX -	WV	RQAPGQGLEWMGXIXPY -	XGXT
HH2	... Q	VQLQESGPGLVKPSQTLSLITCXVSGSXSSXXXXWI	RQ	PPGKGLEWIGXIYYRAXXGXT	
HH3	... E	VOLVQSGGGLVQPGGLSRLISCAASGFTFSXYMX -	WV	RQAPGKGLEWVXXIXXXXGXT	

Germline Consensus (with JH4) :

hVH1	QVQLQSGAEVVKPGASVKVSCKASGYTFGYMH -	WV	RQAPGQGLEWMGWINP -	NSGGT
hVH1I	QITLKESGPTLVKPTQTLTLCTFSGFSLSTSCKGYGVGWIRQPPGKALEWLALIY -	-	-	WNDDK
hVH1II	EVOLVQSGGGLVQPGGLSRLISCAASGFTFSSYIAMS -	WV	RQAPGKGLEWVANIK --	QDGSEK
hVH1V	QVQLQESGPGLVKPSQTLSLITCAVSGSISSNNWW -	SV	VROPPGKGLEWIGEIY --	HSGST
hVHVV	EVOLVQSGAEVVKPGESLKSCKGSGSYFSETSYIWIG --	WV	RQMPGKGLEWLGRTYY -	GDSDT
hVHVI	QVQLQQSGGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWI	WV	QSPSRGLEWLGRYY -	RSKWN
hVHVI	QVQLQSGGSELKKPGASVKVSCKASGYFTSYAMN -	WV	RQAPGQGLEWMGWINT -	NTGNP

FIG. 24B

HEAVY CHAIN carboxy half

SYNPSLKSRSITRDTSKNQFFLQLNISVTTEDTATYCCASFDYAHAM-----DYWGQGTSVTVSS

Pos ... 60_ 70_ 80_ abc 90_ 100_abcdefghijk 110_

Kabat:

HH1 ... NYAQKFQGRVTITDXSTSITAYMELSSLRSXDTAVYCCARXXXXXXXXXXXXXXFDXWGQGTLVTVSS
 HH2 ... XYNPSLKSRSVTISVDTSKNQFSLXLXSVTAAADTAVYCCARXXXXXXXXXXXXXXFDXWGQGTLVTVSS
 HH3 ... YYADSVKGRFTISRDNSKNTLYLQMNLSLRAEDTAVYCCARXXXXXXXXXXXXXXFDXWGQGTLVTVSS

Germline Consensus (with JH4) :

hVHI NYAQKFQGRVTMTRDTSIISTAYMELSSLRSDDTAVYCCARXXXXXXXXXXXXFDYWGQGTLVTVSS
 hVHII RYSPSLKSRSRLTITKDTSKNQVVLTMNMDPVDTATYCCARXXXXXXXXXXXXFDYWGQGTLVTVSS
 hVHII YYVDSVKGRFTISRDNAKNSLYLQMNLSLRAEDTAVYCCARXXXXXXXXXXXXFDYWGQGTLVTVSS
 hVHIV NYNPSLKSRSVTISVDTSKNQFSLKLSSVTAAADTAVYCCARXXXXXXXXXXXXFDYWGQGTLVTVSS
 hVHV RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYCCARXXXXXXXXXXXXFDYWGQGTLVTVSS
 hVHVI DYAVSVKSRITINPDTSKNQFSLQLNISVTPEDTAVYCCARXXXXXXXXXXXXFDYWGQGTLVTVSS
 hVHVI TYAQGFTGRFVFSLDTSVSTAYLQICSLKAEDTAVYCCARXXXXXXXXXXXXFDYWGQGTLVTVSS

Figure 24C:**Kabat numbering of 5H4:****5H4 heavy chain protein sequence:**

1-30: EIQLQQSGPE LVKTGTSVKI SCKASGYSFT
31-35: GYFMH
36-49: WVVKQSHGKSLEWIG
50-65: YIS C (52A) YNGDTNY NQNFKG
66-94: KATF TVDTSSTAY MQF N (82A) S (82B) L (82C) TSED SAVYYCAR
95-102: EGNNYPAY
103-437: WGQG TLTVTVSAAKT TPPSVYPLAP GSAAQTNNSMV
TLGCLVKGYFPEPVTVWNS GSLSGGVHTF PAVLQSDLYT LSSSVTVPSS TWPSETVTCN
VAHPASSTKV DKKIVPRDCG CKPCICTVPE VSSVFIFFFFPK PKDVLTTITLT PKVTCVVVDI
SKDDPEVQFS WFVDDDEVHT AQTQPREEQF NSTFRSVSEL PIMHQDWLNG KEFKCRVNSA
AFFAPIEKTI SKTKGRPKAP QVYTI PPPKE QMAKDKVSLT CMITDFFPED ITVEWQWNGQ
PAENYKNTQP IMDTDGSYFV YSKLNVQKSN WEAGNTFTCS VLHEGLHNHH TEKSLSHSPG K

5H4 light chain protein sequence:

1-23: DIVMTQSHKF MSTSVGDRVT ITC
24-34: KASQNVG TAVT
35-49: WYQQKPGQSPKLLIY
50-56: WTSTRHA
57-88: GVPD RFTGSGSGTD FTLTISDVQS EDLADYFC
89-97: QQYSSYPLT
98-214: FGAGTKLELKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVWKI
DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
STSPIVKSFN RNEC

Figure 24D:**Kabat numbering of MC1****MC-1 heavy chain protein sequence:**

1-30: EVKLVESGGG LVQPGGSLKL SCATSGFTFS
31-35: DYYMY
36-49: WVRQTPEKRLEWVA
50-65: YIS N (52A) GGGSTYY PDTVKKG
66-94: RFTI SRDNNAKNTLY LQM S (82A) R (82B) L (82C) KSED TAMYYCAR
95-102: QGSYGYPPFAY
103-449: WG QGTLVTVSAA KTTAPSVDYPL APVCGDTTGS SVTLGCLVKG YFPEPVTLTW
NSGSLSSGVH TFPAVLQLSDL YTLSSSVTVT SSTWPSQSIT CNVAHPASST KVDKKIEPRG
PTIKPCPPCK CPAPNLLGGP SVFIFPPKIK DVLMISSLSPV VTCVVVDVSE DDPDVQISWF
VNNVEVHTAQ TOTHREDYNS TLRVVVSALPI QHQDWMSGKE FKCKVNNKDL PAPIERTISK
PKGSVRAPQV YVLPPPEEEM TKKQVTLTCM VTDFMPEDIY VEWTNNGKTE LNYKNTEPVL
DSDGSYFMYK KLRVEKKNWV ERNSYSCSVV HEGLHNHHTT KSFSRTPGK

MC-1 light chain protein sequence:

1-23: AIQMTQTTSS LSASLGDRVT ISC
24-34: SASQGIS NYLN
35-49: WYQQKDP DGTVKLLIY
50-56: YTSSLHS
57-88: GVPS RFSGSGSGTD YSLTISNLEP EDIATYYC
89-97: QQ YSKLPWT
98-214: FGGGKLEIKRAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVWKI
DGSERQNGVL NSWTQDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT STSPIVKSFN
RNEC

Figure 24E**Kabat numbering of MC3****MC-3 heavy chain protein sequence:**

1-30: DVQLQESGPG LVKPSQSLSL TCTVTGYSIT
31-35: SDYAW N (35A)
36-49: WIRQ FPGNKLEWMG
50-65: YISYSGSTSY NPSLKS
66-94: RISIT RDTSKNQFFL QL N (82A) S (82B) V (82C) TTEDT ATYYCAR
95-102: LETWLFDY

103-522: WGQG TTLTVSSAKT TPPSVYPLAP GCGDTTGSSV TLGCLVKGYF PESVTVTWNS
GSLSSSVHTF PALLQSGLYT MSSSVTPSS TWPSQTVTCS VAHPASSTTV
DKKLEPSGPI STINPCPPCK ECHKCPAPNL EGGPSVFIFP PNIKDVLMIS
LTPKVTCVVV DVSEDDPDVQ ISWFVNNVEV HTAQQTQTHRE DYNSTIRVVS
TLPIQHQDWL SGKEFKCKVN NKDLPSPIER TISKIKGLVR APQVYILPPP
AEQLSRKDVS LTCLVVGFNP GDISVEWTSN GHTEENYKDT APVLDSDGSY
FIYSKLNMKT SKWEKTDTSFS CNVRHEGLKN YYLKKTISRS PGQLDDICA
EAKDGELEDGL WTTITIFISL FLLSVCYSAS VTLFKVWKIF SSVVELKQKI
SPDYRNMIGQ GA

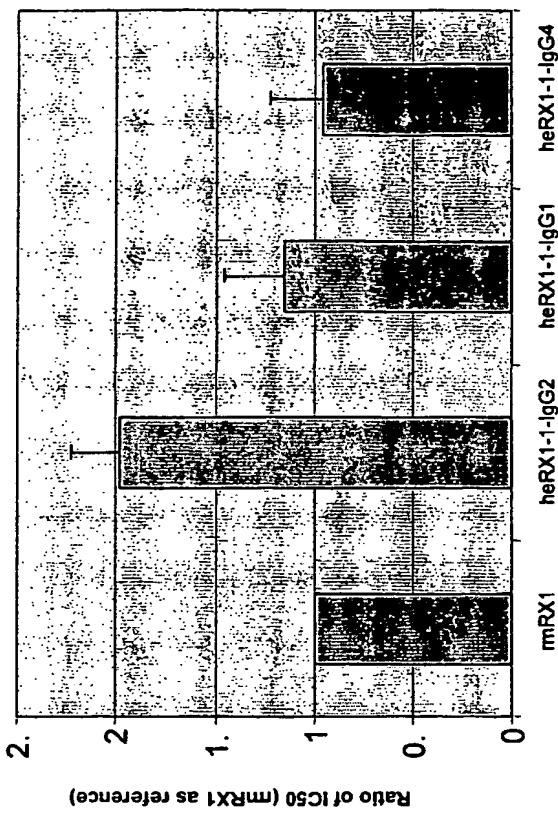
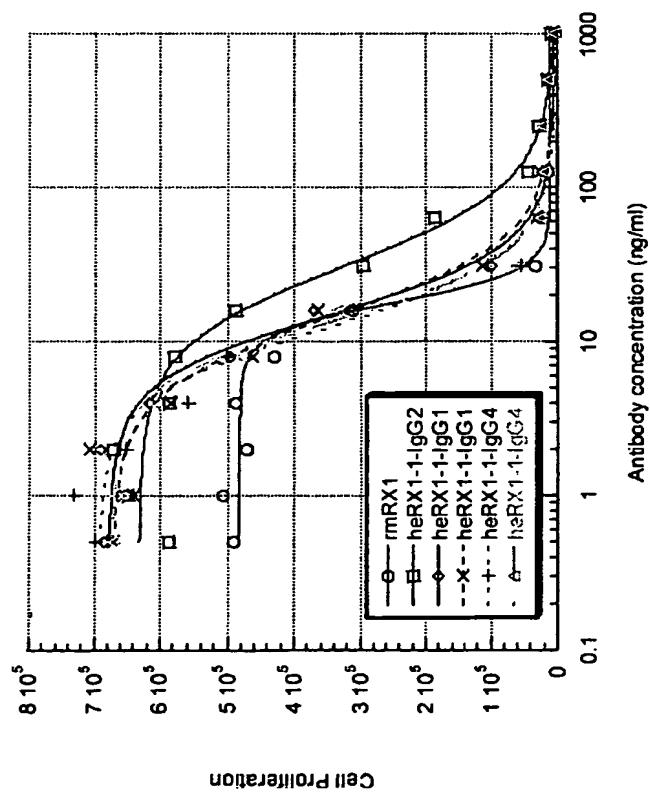
MC-3 light chain protein sequence:

1-23: DILLTQSPA I LSVSPGERVS FSC
24-34: RASQSIG TSIH
35-49: WYQQRT NGSPRLLIK
50-56: YASESIS
57-88: GIPS RFSGSGSGTD FTLSINSVES EDIADYYC
89-97: QQ SNSWPTT
98-214: FGG GTKLEIKWAD AAPTVSIFPP SSEQLTSGGA SVVCFLNNFY PKDINVWKI
DGSERQNGVL NSWTDQDSKD STYSMSSTLT LTKDEYERHN SYTCEATHKT
STSPIVKSFN RNEC

Fig. 25

Measurement of Neutralizing Activity of heRX1 With Different IgG Subclass Constant Regions

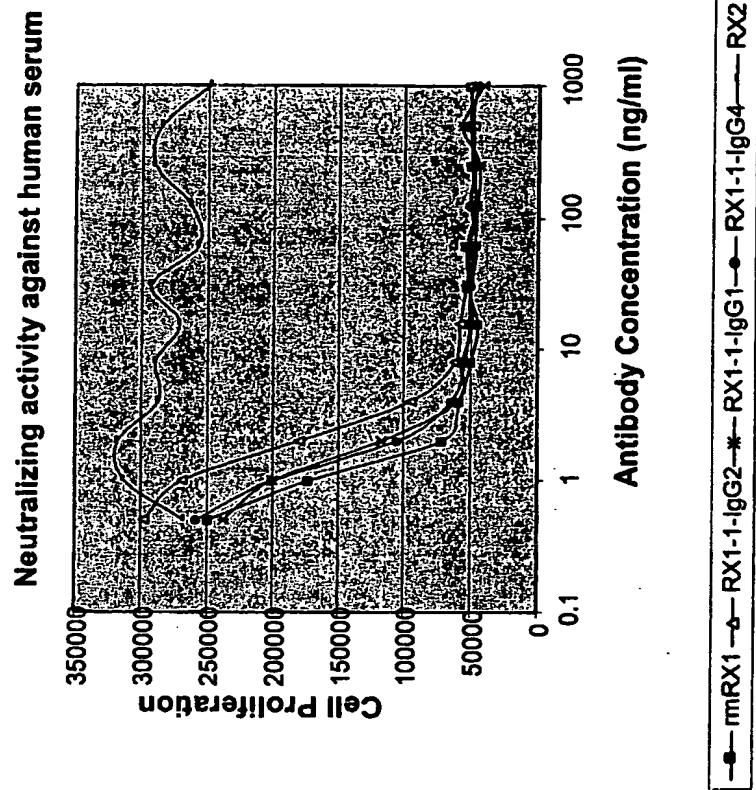
Neutralizing activity of heRX1-1 series



Against recombinant human MCSF

Fig. 26

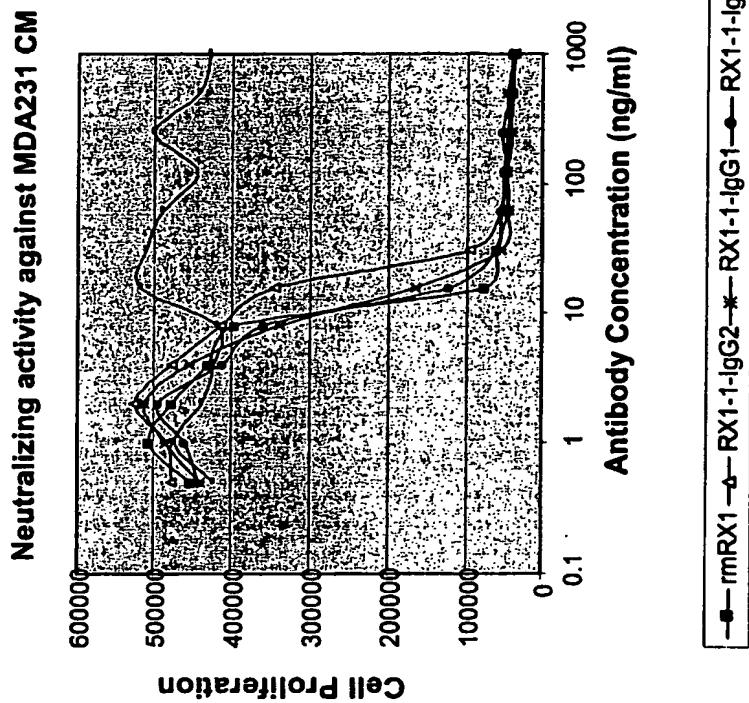
Activity of heRX1-1 With Different IgG Subclasses Against Other Forms of MCSF



Similar results observed against Cyno MCSF in serum and recombinant Cyno MCSF

Fig. 27

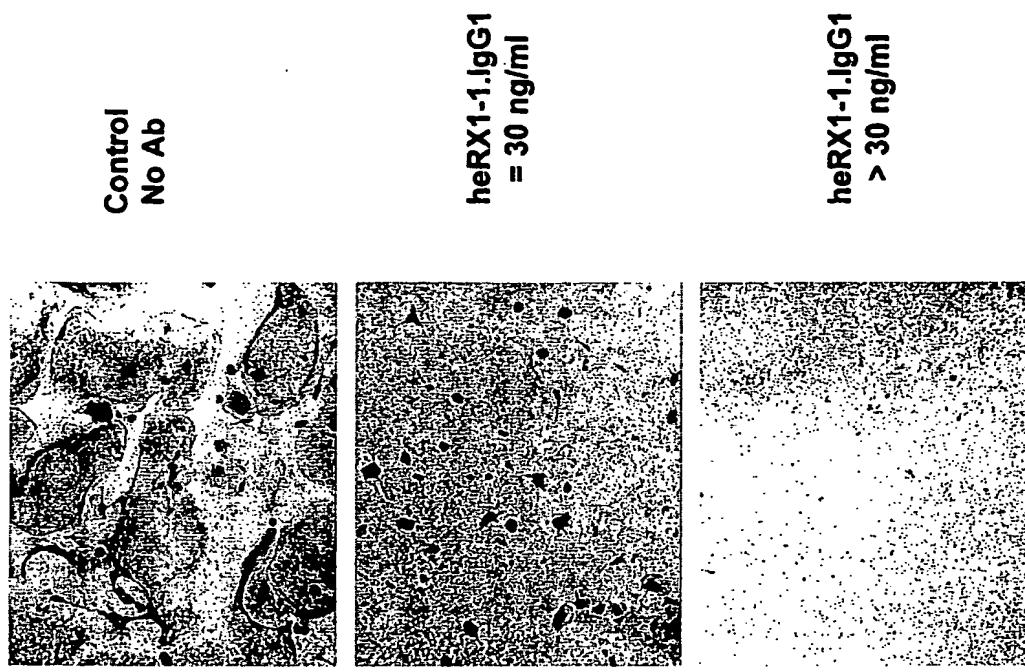
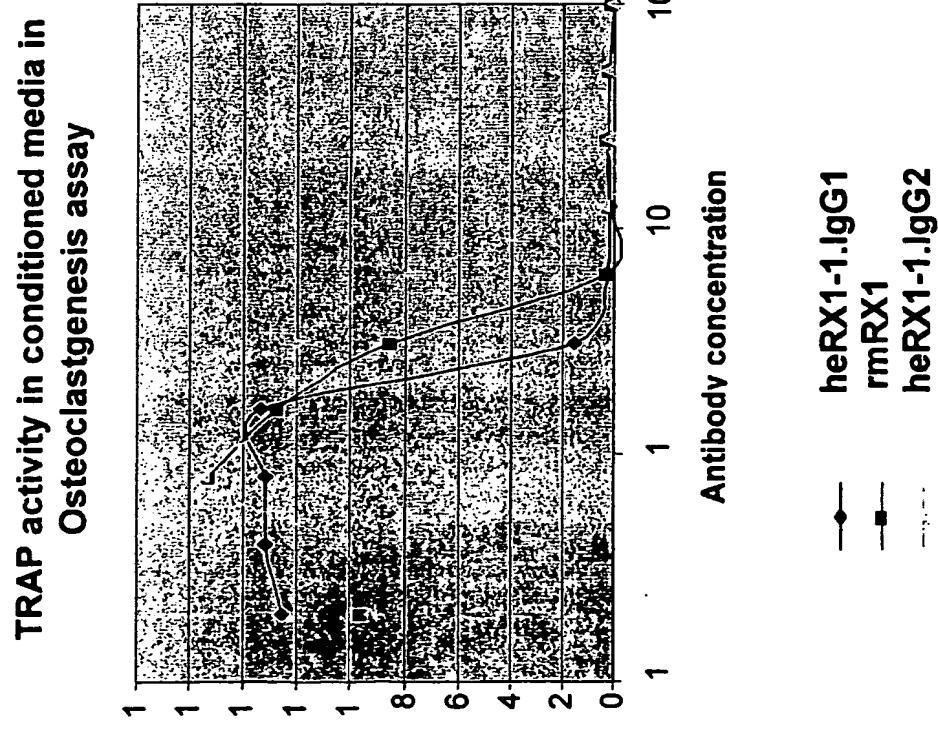
Activity of heRX1-1 With Different IgG Subclasses Against Other Forms of MCSF



Similar results observed against Cyno MCSF in serum and recombinant Cyno MCSF

Fig. 28

osteoclastogenesis Assay of heRX1-1 With Different IgG Subclasses



Amino Acids**MGWSCHILFLVATATGVHS**DVQLQESGPLVKPSQTLSLTCTVTDYSITSDYAWNWRQFPGKKLEWMGYISYSGSTSYNPSLKSRTISRDTSKNQFSL
QLNSVTAADTATYYCASFDYAHAMDYWQGTTVTVSSASTKGPSVFPLAPSSKSTSGTAALGCLVKDYFPEPVTVWSNSGALTSGVHTFPALQSSGLYSLSSVVTVPSSSLGTQTY
ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNNAKTPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNH
YTQKSLSLSPGK.**Nucleotides**ATGGGATGGAGTTGCATTATACTTTCTCGTTGCCACCGCCACTGGAGTTCACTCTGACGTACAACCTCAAGAAC
TGGCCCAGGTCTCGTCAAACCTCTCAAACACTCTCACTCACCTGCACTGTTACTGACTACTCTATTACATCCGACTA
CGCTTGGAACTGGATCCGACAAATTCTCTGGTAAAAAAACTCGAATGGATGGGTTATATTCTTACTCTGGCTCCACCT
CCTACAATCCTCTCTGAAATCACGATCACAAATTCCCGCGATACCTCTAAAATCAATTTCACCTCAACTCAATT
CTGTTACCGCCGCCGATACTGCCACCTACTACTGTGCCTCTTTGACTACGCTCACGCCATGGATTATTGGGGACAG
GGTACTACCGTTACCGTAAGCTCAGCCAGCACAAAGGGCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCA
CCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACTC
AGGCGCCCTGACCAAGCGCGTGCACACCTTCCCGCTGTCCTACAGTCTCAGGACTCTACTCCCTAGCAGCGTGG
TGACCGTGCCCTCCAGCAGCTGGGACCCAGACCTACATCTGCAACGTGAATACAAGCCCAGCAACACCAAGGT
GGACAAGAGAGTTGAGCCAAATCTGTGACAAACTCACACATGTCCACCGTCCCCAGCACCTGAACCTCTGGGG
GGACCGTCAGTCTCCTCTTCCCCCAAAACCCAAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCGT
GGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
CAAGACAAAGCCGCCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACCAAGGA
CTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCC
AAAGCCAAAGGCAGCCCCGAGAACCAACAGGTGACACCCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACAG
GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATGCCGTGGACTCCGACGGCTCTTCTTCTATAGCA
AGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTATGCTCCGTATGCTGATGAGGCTCTGCACAACCAACTACACGCAGA
AGAGCCTCTCCCTGTCCCCGGGTAAATGA

Amino Acids**MGWSCIILFLVATATGVHS**QVQLQESGPGLVKPSQTLSTCTVSDYSITSDYAWNWIQFPKGLEWMGYISYSGSTSYNPSLKSRTISRDTSKNQFSL
QLNSVTAADTAVYYCASFDYAHAMDYWGQGTTVTVSSASTKGPSVFPAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
ICNVNHKPSNTKVDKRVEPKSCDKHTCPVPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAAKTPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNH
YTQKSLSLSPGK.**Nucleotides**ATGGGTTGGCTTGATCATTCCTTCTCGCTACCGCAACTGGTGTACACTCCCAAGTTCAACTTCAAGAATCA
GGCCCCGGACTCGTTAACCCCTCTCAAACCTCTCTTACTTGACTGTATCCGATTACTCTATTACTCAGACTAC
GCTTGGAACTGGATCAGACAATTCCCGAAAAGGACTCGAATGGATGGATATATCTCTTACTCTGGCTCAACCT
CTTACAACCCCTCTCAAATCTCGAATAACAATCTCACGCGATACTTCTAAAAATCAATTCTCACTTCAACTTAAAC
TCCGTTACTGCCGCCACACTGCCGTTACTACTGTGCTTCCTCGATTACGCCACGCTATGGATTATTGGGACA
AGGAACCTACCGTCACTGTCAGCTCAGCCAGCACAAAGGGCCATCGGTCTCCCCCTGGCACCCCTCTCCAAGAGC
ACCTCTGGGGGACAGCGGCCCTGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACT
CAGGCGCCCTGACCAGCGCGTGCACACCTCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTG
GTGACCGTGCCCTCCAGCAGCTGGCACCCAGACCTACATCTGCAACGTGAATACAAGCCCAGCAACACCAAGG
TGGACAAGAGAGTTGAGCCAAATCTTGACAAAAACTCACACATGTCCACCGTGCCTGACCTGAACCTCTGGG
GGGACCGTCAGTCTCCTCTTCCCCCAAAACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCG
TGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGGTGCATAATG
CCAAGACAAAGCCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTACCGTCTGCACCAAGG
ACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTC
CAAAGCCAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCTGAGGAGATGACCAAGAACCA
GGTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGCGACATGCCGTGGAGTGGAGAGCAATGGCAGCCG
GAGAACAACTACAAGACCACGCCCTCCCGTGTGGACTCCGACGGCTCTTCTTCTATAGCAAGCTCACCGTGG
ACAAGAGCAGGTGGCAGCAGGGGAACGTCTCATGCTCCGTATGCATGAGGCTCTGCACAAACCAACTACAGCA
GAAAGAGCCTCTCCCTGTCCCCGGTAAATGA

Fig. 30**HeRX-1 Low Risk Heavy Chain Gamma-4****Amino Acids**

MGWSCIILPEVATATGVHSDVQLQESGPLVKPSQTLSLTCTVTDYSITSVDYAWNWIHQFPGKKLEWMGYISYSGSTSNT
 PSLKSRITISRDTSKNQFLQLNSVTAADTATYYCASFDYAHAMDYWGQGTTVSSASTKGPSVFLAPCSRSTSESTA
 ALGCLVKDYPPEPVTVWSNSGALTSGVHTFPALQSSGLYSLSSVTPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKY
 GPPCPSCPAPEFLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGEVHNAKTKPREEQFNSTYRV
 VSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEW
 ESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHTQKSLSLSLGK

Nucleotides**cDNA**

ATGGGATGGAGTTGCATTATACTTTCTCGTTGCCACCGCCACTGGAGTTCACTCTGACGTACAACCTCAAGAAC
 TGGCCAGGTCTCGTCAAACCTCTCAAACACTCTCACTCACCTGCACTGTTACTGACTACTCTATTACATCCGACTA
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